

RAW SEQUENCE LISTING

**The Biotechnology Systems Branch of the Scientific and Technical
Information Center (STIC) no errors detected.**

Application Serial Number: 09/937,779B
Source: 1FW/b
Date Processed by STIC: 6/13/06

ENTERED



IFW16

RAW SEQUENCE LISTING

DATE: 06/13/2006

PATENT APPLICATION: US/09/937,779B

TIME: 09:45:31

Input Set : A:\00930003.APP

Output Set: N:\CRF4\06132006\I937779B.raw

3 <110> APPLICANT: DAHLQVIST, ANDERS
 4 STAHL, ULF
 5 LENMAN, MARIT
 6 BANAS, ANTONI
 7 RONNE, HANS
 8 STYMNE, STEN
 10 <120> TITLE OF INVENTION: PROCESSES FOR PRODUCING TRIACYLGLYCEROL USING GENES
 11 THAT ENCODE PHOSPHOLIPID:DIACYLGLYCEROL
 12 ACYLTRANSFERASES
 14 <130> FILE REFERENCE: 0093/000003
 16 <140> CURRENT APPLICATION NUMBER: 09/937,779B
 17 <141> CURRENT FILING DATE: 2002-07-02
 19 <150> PRIOR APPLICATION NUMBER: PCT/EP00/002701
 20 <151> PRIOR FILING DATE: 2000-03-28
 22 <150> PRIOR APPLICATION NUMBER: 60/180,687
 23 <151> PRIOR FILING DATE: 2000-02-07
 25 <150> PRIOR APPLICATION NUMBER: EP 99111321.8
 26 <151> PRIOR FILING DATE: 1999-06-10
 28 <150> PRIOR APPLICATION NUMBER: EP 99106656.4
 29 <151> PRIOR FILING DATE: 1999-04-01
 31 <160> NUMBER OF SEQ ID NOS: 35
 33 <170> SOFTWARE: PatentIn Ver. 3.3
 35 <210> SEQ ID NO: 1
 36 <211> LENGTH: 1986
 37 <212> TYPE: DNA
 38 <213> ORGANISM: Saccharomyces cerevisiae
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 42 <222> LOCATION: (1)..(1983)
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 47 1 5 10 15
 49 gat gaa aac aat aaa ggg ggt tct gtt cat aac aag cga gag agc aga 96
 50 Asp Glu Asn Asn Lys Gly Gly Ser Val His Asn Lys Arg Glu Ser Arg
 51 20 25 30
 53 aac cac att cat cat caa cag gga tta ggc cat aag aga aga agg ggt 144
 54 Asn His Ile His His Gln Gln Gly Leu Gly His Lys Arg Arg Arg Gly
 55 35 40 45
 57 att agt ggc agt gca aaa aga aat gag cgt ggc aaa gat ttc gac agg 192
 58 Ile Ser Gly Ser Ala Lys Arg Asn Glu Arg Gly Lys Asp Phe Asp Arg
 59 50 55 60
 61 aaa aga gac ggg aac ggt aga aaa cgt tgg aga gat tcc aga aga ctg 240

P.6

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62 Lys Arg Asp Gly Asn Gly Arg Lys Arg Trp Arg Asp Ser Arg Arg Leu
63 65 70 75 80
65 att ttc att ctt ggt gca ttc tta ggt gta ctt ttg ccg ttt agc ttt 288
66 Ile Phe Ile Leu Gly Ala Phe Leu Gly Val Leu Leu Pro Phe Ser Phe
67 85 90 95
69 ggc gct tat cat gtt cat aat agc gat agc gac ttg ttt gac aac ttt 336
70 Gly Ala Tyr His Val His Asn Ser Asp Ser Asp Leu Phe Asp Asn Phe
71 100 105 110
73 gta aat ttt gat tca ctt aaa gtg tat ttg gat gat tgg aaa gat gtt 384
74 Val Asn Phe Asp Ser Leu Lys Val Tyr Leu Asp Asp Trp Lys Asp Val
75 115 120 125
77 ctc cca caa ggt ata agt tcg ttt att gat gat att cag gct ggt aac 432
78 Leu Pro Gln Gly Ile Ser Ser Phe Ile Asp Asp Ile Gln Ala Gly Asn
79 130 135 140
81 tac tcc aca tct tct tta gat gat ctc agt gaa aat ttt gcc gtt ggt 480
82 Tyr Ser Thr Ser Ser Leu Asp Asp Leu Ser Glu Asn Phe Ala Val Gly
83 145 150 155 160
85 aaa caa ctc tta cgt gat tat aat atc gag gcc aaa cat cct gtt gta 528
86 Lys Gln Leu Leu Arg Asp Tyr Asn Ile Glu Ala Lys His Pro Val Val
87 165 170 175
89 atg gtt cct ggt gtc att tct acg gga att gaa agc tgg gga gtt att 576
90 Met Val Pro Gly Val Ile Ser Thr Gly Ile Glu Ser Trp Gly Val Ile
91 180 185 190
93 gga gac gat gag tgc gat agt tct gcg cat ttt cgt aaa cgg ctg tgg 624
94 Gly Asp Asp Glu Cys Asp Ser Ser Ala His Phe Arg Lys Arg Leu Trp
95 195 200 205
97 gga agt ttt tac atg ctg aga aca atg gtt atg gat aaa gtt tgt tgg 672
98 Gly Ser Phe Tyr Met Leu Arg Thr Met Val Met Asp Lys Val Cys Trp
99 210 215 220
101 ttg aaa cat gta atg tta gat cct gaa aca ggt ctg gac cca ccg aac 720
102 Leu Lys His Val Met Leu Asp Pro Glu Thr Gly Leu Asp Pro Pro Asn
103 225 230 235 240
105 ttt acg cta cgt gca gca cag ggc ttc gaa tca act gat tat ttc atc 768
106 Phe Thr Leu Arg Ala Ala Gln Gly Phe Glu Ser Thr Asp Tyr Phe Ile
107 245 250 255
109 gca ggg tat tgg att tgg aac aaa gtt ttc caa aat ctg gga gta att 816
110 Ala Gly Tyr Trp Ile Trp Asn Lys Val Phe Gln Asn Leu Gly Val Ile
111 260 265 270
113 ggc tat gaa ccc aat aaa atg acg agt gct gcg tat gat tgg agg ctt 864
114 Gly Tyr Glu Pro Asn Lys Met Thr Ser Ala Ala Tyr Asp Trp Arg Leu
115 275 280 285
117 gca tat tta gat cta gaa aga cgc gat agg tac ttt acg aag cta aag 912
118 Ala Tyr Leu Asp Leu Glu Arg Arg Asp Arg Tyr Phe Thr Lys Leu Lys
119 290 295 300
121 gaa caa atc gaa ctg ttt cat caa ttg agt ggt gaa aaa gtt tgt tta 960
122 Glu Gln Ile Glu Leu Phe His Gln Leu Ser Gly Glu Lys Val Cys Leu
123 305 310 315 320
125 att gga cat tct atg ggt tct cag att atc ttt tac ttt atg aaa tgg 1008
126 Ile Gly His Ser Met Gly Ser Gln Ile Ile Phe Tyr Phe Met Lys Trp

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131				340					345					350				
133	aac	gaa	cac	ata	gat	tca	ttc	att	aat	gca	gca	ggg	acg	ctt	ctg	ggc		1104
134	Asn	Glu	His	Ile	Asp	Ser	Phe	Ile	Asn	Ala	Ala	Gly	Thr	Leu	Leu	Gly		
135				355					360					365				
137	gct	cca	aag	gca	gtt	cca	gct	cta	att	agt	ggg	gaa	atg	aaa	gat	acc		1152
138	Ala	Pro	Lys	Ala	Val	Pro	Ala	Leu	Ile	Ser	Gly	Glu	Met	Lys	Asp	Thr		
139				370					375					380				
141	att	caa	tta	aat	acg	tta	gcc	atg	tat	ggg	ttg	gaa	aag	ttc	ttc	tca		1200
142	Ile	Gln	Leu	Asn	Thr	Leu	Ala	Met	Tyr	Gly	Leu	Glu	Lys	Phe	Phe	Ser		
143	385								390					395				400
145	aga	att	gag	aga	gta	aaa	atg	tta	caa	acg	tgg	ggg	ggg	ata	cca	tca		1248
146	Arg	Ile	Glu	Arg	Val	Lys	Met	Leu	Gln	Thr	Trp	Gly	Gly	Ile	Pro	Ser		
147				405					410					415				
149	atg	cta	cca	aag	gga	gaa	gag	gtc	att	tgg	ggg	gat	atg	aag	tca	tct		1296
150	Met	Leu	Pro	Lys	Gly	Glu	Glu	Val	Ile	Trp	Gly	Asp	Met	Lys	Ser	Ser		
151				420					425					430				
153	tca	gag	gat	gca	ttg	aat	aac	aac	act	gac	aca	tac	ggc	aat	ttc	att		1344
154	Ser	Glu	Asp	Ala	Leu	Asn	Asn	Asn	Thr	Asp	Thr	Tyr	Gly	Asn	Phe	Ile		
155				435					440					445				
157	cga	ttt	gaa	agg	aat	acg	agc	gat	gct	ttc	aac	aaa	aat	ttg	aca	atg		1392
158	Arg	Phe	Glu	Arg	Asn	Thr	Ser	Asp	Ala	Phe	Asn	Lys	Asn	Leu	Thr	Met		
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161	aaa	gac	gcc	att	aac	atg	aca	tta	tcg	ata	tca	cct	gaa	tgg	ctc	caa		1440
162	Lys	Asp	Ala	Ile	Asn	Met	Thr	Leu	Ser	Ile	Ser	Pro	Glu	Trp	Leu	Gln		
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165	aga	aga	gta	cat	gag	cag	tac	tcg	ttc	ggc	tat	tcc	aag	aat	gaa	gaa		1488
166	Arg	Arg	Val	His	Glu	Gln	Tyr	Ser	Phe	Gly	Tyr	Ser	Lys	Asn	Glu	Glu		
167				485					490					495				
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170	Glu	Leu	Arg	Lys	Asn	Glu	Leu	His	His	Lys	His	Trp	Ser	Asn	Pro	Met		
171				500					505					510				
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174	Glu	Val	Pro	Leu	Pro	Glu	Ala	Pro	His	Met	Lys	Ile	Tyr	Cys	Ile	Tyr		
175				515					520					525				
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178	Gly	Val	Asn	Asn	Pro	Thr	Glu	Arg	Ala	Tyr	Val	Tyr	Lys	Glu	Glu	Asp		
179				530					535					540				
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183	545								550					555				560
185	gta	ttc	ctc	acc	gag	ggg	gac	gga	acc	gtt	ccg	ctc	gtg	gcg	cat	tca		1728
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189	atg	tgt	cac	aaa	tgg	gcc	cag	ggg	gct	tca	ccg	tac	aac	cct	gcc	gga		1776
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197 ata cgt ggt gga gca aaa agc gcc gaa cac gta gac atc ctc ggc agc 1872
198 Ile Arg Gly Gly Ala Lys Ser Ala Glu His Val Asp Ile Leu Gly Ser
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201 gcg gag ttg aac gat tac atc ttg aaa att gca agc ggt aat ggc gat 1920
202 Ala Glu Leu Asn Asp Tyr Ile Leu Lys Ile Ala Ser Gly Asn Gly Asp
203 625          630          635          640
205 ctc gtc gag cca cgc caa ttg tct aat ttg agc cag tgg gtt tct cag 1968
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227          35          40          45
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230          50          55          60
232 Lys Arg Asp Gly Asn Gly Arg Lys Arg Trp Arg Asp Ser Arg Arg Leu
233    65          70          75          80
235 Ile Phe Ile Leu Gly Ala Phe Leu Gly Val Leu Leu Pro Phe Ser Phe
236          85          90          95
238 Gly Ala Tyr His Val His Asn Ser Asp Ser Asp Leu Phe Asp Asn Phe
239          100          105          110
241 Val Asn Phe Asp Ser Leu Lys Val Tyr Leu Asp Asp Trp Lys Asp Val
242          115          120          125
244 Leu Pro Gln Gly Ile Ser Ser Phe Ile Asp Asp Ile Gln Ala Gly Asn
245          130          135          140
247 Tyr Ser Thr Ser Ser Leu Asp Asp Leu Ser Glu Asn Phe Ala Val Gly
248 145          150          155          160
250 Lys Gln Leu Leu Arg Asp Tyr Asn Ile Glu Ala Lys His Pro Val Val
251          165          170          175
253 Met Val Pro Gly Val Ile Ser Thr Gly Ile Glu Ser Trp Gly Val Ile
254          180          185          190
256 Gly Asp Asp Glu Cys Asp Ser Ser Ala His Phe Arg Lys Arg Leu Trp
257          195          200          205
259 Gly Ser Phe Tyr Met Leu Arg Thr Met Val Met Asp Lys Val Cys Trp
260          210          215          220
262 Leu Lys His Val Met Leu Asp Pro Glu Thr Gly Leu Asp Pro Pro Asn

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263	225				230				235				240			
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269				260					265					270		
271	Gly	Tyr	Glu	Pro	Asn	Lys	Met	Thr	Ser	Ala	Ala	Tyr	Asp	Trp	Arg	Leu
272			275					280					285			
274	Ala	Tyr	Leu	Asp	Leu	Glu	Arg	Arg	Asp	Arg	Tyr	Phe	Thr	Lys	Leu	Lys
275		290					295					300				
277	Glu	Gln	Ile	Glu	Leu	Phe	His	Gln	Leu	Ser	Gly	Glu	Lys	Val	Cys	Leu
278	305				310					315					320	
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284			340						345					350		
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287			355					360					365			
289	Ala	Pro	Lys	Ala	Val	Pro	Ala	Leu	Ile	Ser	Gly	Glu	Met	Lys	Asp	Thr
290		370					375					380				
292	Ile	Gln	Leu	Asn	Thr	Leu	Ala	Met	Tyr	Gly	Leu	Glu	Lys	Phe	Phe	Ser
293	385				390					395					400	
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296				405					410						415	
298	Met	Leu	Pro	Lys	Gly	Glu	Glu	Val	Ile	Trp	Gly	Asp	Met	Lys	Ser	Ser
299			420					425					430			
301	Ser	Glu	Asp	Ala	Leu	Asn	Asn	Asn	Thr	Asp	Thr	Tyr	Gly	Asn	Phe	Ile
302			435					440					445			
304	Arg	Phe	Glu	Arg	Asn	Thr	Ser	Asp	Ala	Phe	Asn	Lys	Asn	Leu	Thr	Met
305		450					455					460				
307	Lys	Asp	Ala	Ile	Asn	Met	Thr	Leu	Ser	Ile	Ser	Pro	Glu	Trp	Leu	Gln
308	465				470					475					480	
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311				485					490						495	
313	Glu	Leu	Arg	Lys	Asn	Glu	Leu	His	His	Lys	His	Trp	Ser	Asn	Pro	Met
314				500					505					510		
316	Glu	Val	Pro	Leu	Pro	Glu	Ala	Pro	His	Met	Lys	Ile	Tyr	Cys	Ile	Tyr
317		515						520					525			
319	Gly	Val	Asn	Asn	Pro	Thr	Glu	Arg	Ala	Tyr	Val	Tyr	Lys	Glu	Glu	Asp
320		530					535					540				
322	Asp	Ser	Ser	Ala	Leu	Asn	Leu	Thr	Ile	Asp	Tyr	Glu	Ser	Lys	Gln	Pro
323	545				550					555					560	
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326				565					570						575	
328	Met	Cys	His	Lys	Trp	Ala	Gln	Gly	Ala	Ser	Pro	Tyr	Asn	Pro	Ala	Gly
329				580					585					590		
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332		595					600						605			
334	Ile	Arg	Gly	Gly	Ala	Lys	Ser	Ala	Glu	His	Val	Asp	Ile	Leu	Gly	Ser
335		610					615					620				

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Please Note:

Use of n and/or Xaa have been detected in the Sequence Listing. Please review the Sequence Listing to ensure that a corresponding explanation is presented in the <220> to <223> fields of each sequence which presents at least one n or Xaa.

Seq#:5; N Pos. 2363
Seq#:7; N Pos. 601,627
Seq#:9; N Pos. 15,45,83,103,107,112,210
Seq#:25; N Pos. 240,385
Seq#:25; Xaa Pos. 41,89
Seq#:26; N Pos. 601,627
Seq#:28; N Pos. 15,45,83,103,107,112,210
Seq#:32; Xaa Pos. 2
Seq#:35; Xaa Pos. 41,89

VERIFICATION SUMMARY

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L:515 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:5 after pos.:2340
L:710 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:7 after pos.:565
M:341 Repeated in SeqNo=7
L:788 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:9 after pos.:0
M:341 Repeated in SeqNo=9
L:2328 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:25 after pos.:215
M:341 Repeated in SeqNo=25
L:2404 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:26 after pos.:565
M:341 Repeated in SeqNo=26
L:2482 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:28 after pos.:0
M:341 Repeated in SeqNo=28
L:2636 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:32 after pos.:0
L:2689 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:35 after pos.:32
M:341 Repeated in SeqNo=35